

## SEQUENCE LISTING

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 34 base pairs  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GACTCGCTGC AGATCGATT TTTTTTTTTT TTTT

34

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 30 base pairs  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GCCATCAAGC CACCCAAGAA CTCTTAACCTT

30

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 30 base pairs  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CCAATAGCCA GACCATTATA TACACTAATT

30

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 310 base pairs  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

GCTTATAGAA GGACCCCTAG TATGGGGTAA TCCCCTCTGG GAAACCAAGC CCCACTACTC	60
AGCAGGAAAA ATAGAATAGG AAACCTCACCA AGGACATACT TTCCCTCCCT CCAGATGGCT	120
AGCCACTGAG GAAGGAAAAA TACTTTCAACC TGCACTAAC CACAGAAAT TACTTAAAAC	180
CCTTCACCAA ACCTTCCACT TAGGCATTGA TAGCACCCAT CAGATGGCCA AATTATTATT	240
TACTGGACCA GGCCTTTCA AACTATCAA GAAGATAGTC AGGGGCTGTG AAGTGTGCCA	300
AAGAAATAAT	310

(2) INFORMATION FOR SEQ ID NO: 113:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Leu Ile Glu Gly Pro Leu Val Trp Gly Asn Pro Leu Trp Glu Thr Lys

1 5 10 15

Pro Gln Tyr Ser Ala Gly Lys Ile Glu Xaa Glu Thr Ser Gln Gly His

20 25 30

Thr Phe Leu Pro Ser Arg Trp Leu Ala Thr Glu Glu Gly Lys Ile Leu

35 40 45

Ser Pro Ala Ala Asn Gln Gln Lys Leu Leu Lys Thr Leu His Gln Thr

50 55 60

Phe His Leu Gly Ile Asp Ser Thr His Gln Met Ala Lys Leu Leu Phe

65 70 75 80

Thr Gly Pro Gly Leu Phe Lys Thr Ile Lys Lys Ile Val Arg Gly Cys

85 90 95

Glu Val Cys Gln Arg Asn Asn

100

(2) INFORMATION FOR SEQ ID NO: 114:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

CCCTGTATCT TTAACCTCCT TGTAAAGTTT GTCTCTTCCA GAATCAAAAC TGTAAAAC 60  
CAAATTGTTTC TTCAAATGGA GCACCCAGATG GAGTCCATGA CTAAGATCCA CCGTGGACCC 120  
CTGGACCGGC CTGCTAGCCC ATGCTCCGAT GTTAATGACA TTGAAGGCAC CCCTCCCGAG 180  
GAAATCTCAA CTGCACAACC CCTACTATGC CCCAATTCA CGGGAAAGCAC TTAGAGCGGT 240  
CATCAGCCAA CCTCCCCAAC ACCACTTGGG TTTTCTCTT GAGAGGGGGG ACTGAGAGAC 300  
AGGACTAGCT GGATTTCCTA GGCCAAACGAA GAATCCCTAA CCCTAGCTGG CAAGGTGACT 360  
GCATCCACCT CTAAACATGG GCCTTGCAAC TTAGCTCACA CCCGACCAAT CACAGAGCTC 420  
ACTAAAATGCC TAATTAGGCA AAAATAGGAG GTAAAGAAAT AGCCAATCAT CTATTGCCCTG 480  
AGAGCACACGC GGGAGGGACA AGGATCGGGGATAAAACCA GGCAATTGGAG CCGGCAACGG 540  
CAACCCCCCTT TGGGTCCCCCT CCCTTTGTAT GGGCGCTCTG TTTTCACTCT ATTTCACCT 600  
ATTTAAATCTT GCAACTGAAA AAAAAAAA AAAAAA 635

(2) INFORMATION FOR SEQ ID NO: 115

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

5

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile Lys

1 5 10 15

Thr Val Lys Leu Gln Ile Val Leu Gln Met Glu His Gln Met Glu Ser

20 25 30

Met Thr Lys Ile His Arg Gly Pro Leu Asp Arg Pro Ala Ser Pro Cys

35 40 45

Ser Asp Val Asn Asp Ile Glu Gly Thr Pro Pro Glu Glu Ile Ser Thr

50 55 60

Ala Gln Pro Leu Leu Cys Pro Asn Ser Ala Gly Ser Ser

10

65 70 75

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleotide
- 5 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

TGGGGTTCCA TTTGTAAGAC CATCTGTAGC TT

32

10

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1481 base pairs
- (B) TYPE: nucleotide
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATGGCCCTCC CTTATCATAAC TTTTCTCTTT ACTGTTCTCT TACCCCTTT CGCTCTCACT 60  
GCACCCCCCTC CATGCTGCTG TACAACCAGT AGCTCCCCTT ACCAAGAGTT TCTATGAACA 120  
ACCGGGCTTC CTGGAAATAT TGATGCCCA TCATATAGGA GTTTATCTAA GGGAAACTCC 180  
ACCTTCACTG CCCACACCCA TATGCCCGGC AACTGCTATA ACTCTCCAC TCTTTGCATG 240  
CATGCAAATA CTCATTATTG GACAGGGAAA ATGATTATTC CTAGTTGTCC TGGAGGACTT 300  
GGAGCCACTG TCTGTTGGAC TTACTTCACC CATAACAGTA TGTCTGATGG GGGTGGAAATT 360  
CAAGGTCAGG CAAGAGAAAA ACAACTAAGG GAAGGAAATCT CCCAACTGAC CCGGGGACAT 420  
AGCACCCCTA GCCCCACAA AGGACTAGTT CTCTCAAAAC TACATGAAAC CCTCCGTACC 480  
CATACTCGCC TGGTGAGCCT ATTTAATACC ACCCTCACTC GGCTCCATGA GGTCTCAGCC 540  
CAAAACCTA CTAACGTGTC GATGTGCCTC CCCCTGCACT TCAGGCCATA CATTCAATC 600  
CCTGTTCTG AACAAATGGAA CAACTTCAGC ACAGAAATAA ACACCACTTC CGTTTTAGTA 660  
GGACCTCTTG TTTCCAATCT GGAAATAACG CATAACCTAA ACCTCACCTG TGAAAAATT 720  
AGCAATACTA TAGACACAAAC CAGCTCCGAA TGCATCAGGT GGGTAACACC TCCCACACGA 780  
ATAGTCTGCC TACCCCTCAGG AATAATTITTT GTCTGTTGGTA CCTCAGCCTA TCATTGTTG 840  
AATGGCTCTT CAGAACATAT GTGCTCTCTC TCATTCTTAG TGCCCCCTAT GACCATCTAC 900  
ACTGAACAAG ATTATACAA TCATGTCGTA CCTAAGCCCC ACAACAAAAG AGTACCCATT 960  
CTTCCTTTTG TTATCAGAGC AGGAGTGCTA GCCAGACTAG CTACTGGCAT TGGCAGTATC 1020

20

ACAAACCTCTA CTCAGTTCTA CTACAAACTA TCTCAAGAAA TAAATGGTGA CATCGAACAG 1080  
GTCACTGACT CCCTGGTCAC CTTGCAAGAT CAACTTAAC CCCTAGCACC AGTAGTCCTT 1140  
CAAAATCGAA GAGCTTTAGA CTTGCTAACCC GCCAAAAGAG GGGGAACCTG TTTATTTTTA 1200  
GGAGAAGAAC GCTGTTATTA TGTTAATCAA TCCAGAATTG TCACTGAGAA AGTTAAAGAA 1260  
ATTCGAGATC GAATACAATG TAGAGCAGAG GAGCTCTAAA ACACCGAACG CTGGGGCCTC 1320  
CTCAGCCAAT GGATGCCCTG GGTTCTCCCC TTCTTAGGAC CTCTAGCAGC TCTAATATTG 1380  
TTACTCCTCT TTGGACCCCTG TATCTTTAAC CTCCTGTAA AGTTGTCTC TTCCAGAATT 1440  
GAAGCTGTAA AGCTACAGAT GGTCTTACAA ATGGAACCCC A 1481

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 493 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

Met Ala Leu Pro Tyr His Thr Phe Leu Phe Thr Val Leu Leu Pro Pro  
1 5 10 15  
Phe Ala Leu Thr Ala Pro Pro Pro Cys Cys Cys Thr Thr Ser Ser Ser  
20 25 30  
Pro Tyr Gln Glu Phe Leu Xaa Arg Thr Arg Leu Pro Gly Asn Ile Asp  
35 40 45  
Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Asn Ser Thr Phe Thr Ala  
50 55 60  
His Thr His Met Pro Arg Asn Cys Tyr Asn Ser Ala Thr Leu Cys Met  
65 70 75 80  
His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys  
85 90 95  
Pro Gly Gly Leu Gly Ala Thr Val Cys Trp Thr Tyr Phe Thr His Thr  
100 105 110  
Ser Met Ser Asp Gly Gly Gly Ile Gln Gly Gln Ala Arg Glu Lys Gln  
115 120 125  
Val Lys Glu Ala Ile Ser Gln Leu Thr Arg Gly His Ser Thr Pro Ser  
130 135 140  
Pro Tyr Lys Gly Leu Val Leu Ser Lys Leu His Glu Thr Leu Arg Thr

145                    150                    155                    160  
His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Arg Leu His  
165                    170                    175  
Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Met Cys Leu Pro Leu  
180                    185                    190  
His Phe Arg Pro Tyr Ile Ser Ile Pro Val Pro Glu Gln Trp Asn Asn  
195                    200                    205  
Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val  
210                    215                    220  
Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe  
225                    230                    235                    240  
Ser Asn Thr Ile Asp Thr Thr Ser Ser Gln Cys Ile Arg Trp Val Thr  
245                    250                    255  
Pro Pro Thr Arg Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys  
260                    265                    270  
Gly Thr Ser Ala Tyr His Cys Leu Asn Gly Ser Ser Glu Ser Met Cys  
275                    280                    285  
Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp  
290                    295                    300  
Leu Tyr Asn His Val Val Pro Lys Pro His Asn Lys Arg Val Pro Ile  
305                    310                    315                    320  
Leu Pro Phe Val Ile Arg Ala Gly Val Leu Gly Arg Leu Gly Thr Gly  
325                    330                    335  
Ile Gly Ser Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln  
340                    345                    350  
Glu Ile Asn Gly Asp Met Glu Gln Val Thr Asp Ser Leu Val Thr Leu  
355                    360                    365  
Gln Asp Gln Leu Asn Ser Leu Ala Ala Val Val Leu Gln Asn Arg Arg  
370                    375                    380  
Ala Leu Asp Leu Leu Thr Ala Lys Arg Gly Gly Thr Cys Leu Phe Leu  
385                    390                    395                    400  
Gly Glu Glu Arg Cys Tyr Tyr Val Asn Gln Ser Arg Ile Val Thr Glu  
405                    410                    415  
Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Cys Arg Ala Glu Glu Leu  
420                    425                    430  
Gln Asn Thr Glu Arg Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Val

435

440

445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Leu Ile Leu Leu Leu Leu Phe  
450 455 460  
Gly Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile  
465 470 475 480  
Glu Ala Val Lys Leu Gln Met Val Leu Gln Met Glu Pro  
485 490

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 32 base pairs  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TCAAAATCGA AGAGCTTTAG ACTTGCTAAC CG 32

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1329 base pairs  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

TCAAAATCGA AGAGCTTTAG ACTTGCTAAC CGCCAAAAGA GGGGGAACCT GTTTATTTT 60  
AGGGGAAGAA TGCTGTTAGT ATGTTAATCA ATCTGGAATC ATTACTGAGA AAGTTAAAGA 120  
AATTGAGAT CGAATATAAT GTAGAGCAGA GGACCTTCAA AACACTGCAC CCTGGGGCCT 180  
CCTCAGCCAA TGGATGCCCT GGACTCTCCC CTTCTTAGGA CCTCTAGCAG CTATAATATT 240  
TTTACTCCCT TTGGACCCCT GTATCTTCAA CTTCTTGTAA AAGTTTGTCCTTCCAGAAT 300  
TGAAGCTGTA AAGCTACAAA TAGTTCTCA AATGGAACCC CAGATGCCAGT CCATGACTAA 360  
AATCTACCGT GGACCCCTGG ACCGGCCTGC TAGACTATGC TCTGATGTTA ATGACATTGA 420  
AGTCACCCCT CCCGAGGAAA TCTCAACTGC ACAACCCCTA CTACACTCCA ATTCACTAGG 480  
AAGCAGTTAG AGCAGTTGTC AGCCAACCTC CCCAACAGTA CTTGGTTTT CCTGTTGAGA 540  
GGGTGGACTG AGAGACAGGA CTAGCTGGAT TTCCTAGGCT GACTAAGAAAT CCCNAAGCCT 600

ANCTGGGAAG GTGACCCAT CCATCTTAA ACATGGGCT TGCAACTTAG CTCACACCCC 660  
ACCAATCAGA GAGCTCACTA AAATGCTAAT CAGGCAAAAA CAGGAGGTAAC AGCAATAGCC 720  
AATCATCTAT TGCCTGAGAG CACAGCGGGA AGGACAAGGA TTGGGATATA AACTCAGGCC 780  
TTCAAGCCAG CAACAGCAAC CCCCTTGGA TCCCCCTCCA TTGTATGGGA GCTCTGTTT 840  
CACTCTATT CACTCTATTA AATCATGCAA CTGCACCTT CTGGTCCGTG TTTTTATGG 900  
CTCAAGCTGA GCTTTTGTTC GCCATCCACC ACTGCTGTT GCCACCGTCA CAGACCCGCT 960  
GCTGACTTCC ATCCCTTGGA ATCCAGCAGA GTGTCCACTG TGCTCCTGAT CCAGCGAGGT 1020  
ACCCATTGCC ACTCCCGATC AGGCTAAAGG CTTGCCATTG TTCCCTGCATG GCTAAGTGCC 1080  
TGGGTTTGTGTC CTAATAGAAC TGAACACTGG TCACTGGGTT CCATGGTTCT CTTCCATGAC 1140  
CCACGGCTTC TAATAGAGCT ATAACACTCA CCGCATGGCC CAAGATTCCA TICCTTGGTA 1200  
TCTGTGAGGC CAAGAACCCC AGGTCAGAGA ANGTGAGGCT TGCCACCATT TGGGAAGTGG 1260  
CCCACTGCCA TTTTGGTAGC GCCCCACCAC CATCTTGGGA GCTGTGGGAG CAAGGATCCC 1320  
CCAGTAACA 1329

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 162 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Gln Asn Arg Arg Ala Leu Asp Leu Leu Thr Ala Lys Arg Gly Gly Thr  
1 5 10 15  
Cys Leu Phe Leu Gly Glu Glu Cys Cys Xaa Tyr Val Asn Gln Ser Gly  
20 25 30  
Ile Ile Thr Glu Lys Val Lys Glu Ile Xaa Asp Arg Ile Xaa Cys Arg  
35 40 45  
Ala Glu Asp Leu Gln Asn Thr Ala Pro Trp Gly Leu Leu Ser Gln Trp  
50 55 60  
Met Pro Trp Thr Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Phe  
65 70 75 80  
Leu Leu Leu Phe Gly Pro Cys Ile Phe Asn Phe Leu Val Lys Phe Val  
85 90 95  
Ser Ser Arg Ile Glu Ala Val Lys Leu Gln Ile Val Leu Gln Met Glu  
100 105 110

Pro Gln Met Gln Ser Met Thr Lys Ile Tyr Arg Gly Pro Leu Asp Arg  
115 120 125  
Pro Ala Arg Leu Cys Ser Asp Val Asn Asp Ile Glu Val Thr Pro Pro  
130 135 140  
Glu Glu Ile Ser Thr Ala Gln Pro Leu Leu His Ser Asn Ser Val Gly  
145 150 155 160  
Ser Ser

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs  
5 (B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

10 GGCATTGATA GCACCCATCA G

21

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs  
15 (B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

20 CATGTCACCA GGGTGGAATA G

21

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
25 (B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 758 base pairs  
(B) TYPE: nucleotide  
5 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124.

GGCATTGATA GCACCCATCA GATGCCAAA TCATTATTTA CTGGACCAGG CCTTTTCAA 60  
ACTATCAAGC AGATAAGGCC CGTGAAGCAT GCCAAAGAAA TAATCCCCTG CCTTATCGCC 120  
ATGTTCCCTTC AGGAGAACAA AGAACAGGCC ATTACCCAGG GGAAGACTGG CAACTAGATT 180  
TTACCCACAT GGCCAAATGT CAGGGATTTC AGCATCTACT AGTCTGGGA GATACTTCA 240  
CTGGTTGGGT GGAGTCTTCT CCTTGTAGGA CAGAAAGAC CCAAGAGGTA ATAAAGGCAC 300  
TAATGAAATA ATTCCCAGAT TTGGACTTCC CCCAGGATTA CAGGGTCACA ATGGCCCCGC 360  
TTTCAAGGCT GCAGTAACCC AGGGACTATC CCAGGTGTTA GCCATACAAAT ATCACTTACA 420  
CTGTGCCCTGG AGGCCACAAT CCTCCAGAAA ACTCAAGAAA ATGAATGAAA CACTCAAAGA 480  
TCTAAAAAAAG CTAACCCAAAG AAACCCACAT TGCATGACCT GTTCTTTGC CTATAACCTT 540  
ACTAAGAACATC CATAACTATC CCCCAAAAAG CAGGACTTAG CCCATACGAG ATGCTATATG 600  
GATGGCCTTT CCTAACCAAT GACCTTGTGC TTGACTGAGA AATGGCCAAC TTAGTTGCAG 660  
ACATCACCTC CTTAGCCAAA TATCAACAAG TTCTTAAAC ATCACAGGGG ACCTGTCCCC 720  
GAGAGGAGGG AAAGGAACTA TTCCACCCCTG GTGACATG 758

10 (2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs  
(B) TYPE: nucleotide  
15 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

CGGACATCCA AAGTGATGGG AAACG

25

20 (2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs  
(B) TYPE: nucleotide  
25 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

GGACAGGAAA GTAAGACTGA GAAGGC

26

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 base pairs  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CCTAGAACGT ATTCTGGAGA ATTGGG

26

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 26 base pairs  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

TGGCTCTCAA TGGTCAAACA TACCCG

26

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1511 base pairs  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

~~CCTAGAACGT ATTCTGGAGA ATTGGGACCA ATGTGACACT CAGACGCTAA GAAAGAAACG~~ 60

ATTTATATTCTTCTGCAGTA CGCCCTGGCC ACAATATCCT CTTCAAGGGA GAGAAACCTG 120  
GCTTCCTCGAG CGAACGTATAA ATTATAACAT CATCTTACAG CTACACCTCT TCTGTAGAAA 180  
GGAGGGCAAA TGGAGTGAAG TGCCATATGT GCAAAATTTG TTTTCATTAA GAGACAACTC 240  
ACAATTATGT AAAAAGTGTG GTTATGCC TACAGGAAGC CCTCAGAGTC CACCTCCCTA 300  
CCCCAGCGTC CCCTCCCCGA CTCCCTCCCTC AACTAATAAG GACCCCCCTT TAACCCAAAC 360  
GGTCCAAAAG GAGATAGACA AACGGGTAAA CAATGAACCA AAGAGTGCCA ATATTCCCCG 420  
ATTATGCCCTC CTCCAAGCAG TGAGAGGAGG AGAATTGGC CCAGCCAGAG TGCTGTAC 480  
TTTTCTCTC TCAGACTTAA AGCAAATTAA AATAGACCTA GGTAATTCT CAGATAACCC 540  
TGACGGCTAT ATTGATGTTT TACAAGGGTT AGGACAATCC TTGATCTGA CATGGACAGA 600  
TATAATGTTA CTACTAAATC AGACACTAAC CCCAAATGAG AGAAGTGGCG CTGTAACCTG 660  
ACCCCGAGAG TTTGGCGATC TTTGGTATCT CAGTCAGGCC AACAAATAGGA TGACAACAGA 720  
GGAAAGAACAACTCCCACAG GCCAGCAGGC AGTTCCCAGT GTAGACCCCTC ATTGGGACAC 780  
AGAATCAGAA CATGGAGATT GGTGCCACAA ACATTGCTA ACTTGGGTG TAGAAGGACT 840  
GAGGAAAAGT AGGAAGAACG CTATGAATTAA CTCAATGATG TCCACTATAA CACAGGGAAA 900  
GGAAGAAAAT CTTACTGCTT TTCTGGACAG ACTRAAGGGAG GCATTGAGGA AGCATAACCTC 960  
CCTGTCACCT GACTCTATTG AAGCCAACT AATCTAAAG GATAAGTTA TCACTCAGTC 1020  
ACCTGCCAGAC ATTAGAAAAA ACTTCAAAAG TCTGCCCTAG GCCCGGAGCA GAACCTAGAA 1080  
ACCCCTATTAA ACTTGGCATC CTCAGTTTT TATAATAGAG ATCAGGGAGGA GCAGGGAAA 1140  
CGGGACAAAC GGGATAAAAAA AAAAGGGGG GGTCCACTAC TTAGTCATG GCCCTCAGGC 1200  
AAGCAGACTT TGGAGGCTCT GCAAAAGGGA AAAGCTGGC AAATCAAATG CCTAATAGGG 1260  
CTGGCTTCCA GTGGGTCTA CAAGGACACT TTAAAAAAGA TTATCCAAGT AGAAAATAAGC 1320  
CCCCCCTTG TCCATGGCCC TTACGTCAAG GGAATCCTG GAAGGGCCAC TGCCCCAGGG 1380  
GATGAAGATA CTCTGAGTCA GAAGCCATTAA ACCAGATGAT CCAGCAGCAG GACTGAGGGT 1440  
GCCCGGGGCG AGGCCAGCC CATGCCATCA CCCTCACAGA GCCCCGGGTA TGTTTGACCA 1500  
TTGAGAGCCA A 1511

(2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Leu Glu Arg Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr Leu  
10 1 5 10 15

Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln Tyr  
20 25 30

Pro Leu Gln Gln Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr  
35 40 45

Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp  
50 55 60

Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser  
65 70 75 80

Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser  
85 90 95

Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn  
100 105 110

Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly  
115 120 125

Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu  
130 135 140

Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro  
145 150 155 160

Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe  
165 170 175

Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln  
180 185 190

Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr  
195 200 205

Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe  
210 215 220

Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu  
225 230 235 240

Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro  
245 250 255

His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu  
260 265 270

Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met  
275 280 285

Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu  
290 295 300

1 5 10 15  
Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
20 25 30  
Ile Leu Glu Arg Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr  
35 40 45  
Leu Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln  
50 55 60  
Tyr Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn  
65 70 75 80  
Tyr Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys  
85 90 95  
Trp Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn  
100 105 110  
Ser Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln  
115 120 125  
Ser Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr  
130 135 140  
Asn Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys  
145 150 155 160  
Gly Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro  
165 170 175  
Leu Gln Ala Val Arg Gly Glu Phe Gly Pro Ala Arg Val Pro Val  
180 185 190  
Pro Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys  
195 200 205  
Phe Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly  
210 215 220  
Gln Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln  
225 230 235 240  
Thr Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu  
245 250 255  
Phe Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr  
260 265 270  
Glu Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp  
275 280 285  
Pro His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His

290

295

300

Leu Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro  
305 310 315 320  
Met Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn  
325 330 335  
Leu Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr  
340 345 350  
Ser Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys  
355 360 365  
Phe Ile Thr Gln Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu  
370 375 380  
Pro Lys Leu Ala Ala Ala Leu Glu His His His His His His  
385 390 395

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 378 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Leu Glu Arg  
1 5 10 15  
Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr Leu Arg Lys Lys  
20 25 30  
Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln Tyr Pro Leu Gln  
35 40 45  
Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr Asn Ile Ile  
50 55 60  
Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp Ser Glu Val  
65 70 75 80  
Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser Gln Leu Cys  
85 90 95  
Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser Pro Pro Pro  
100 105 110

10

Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn Lys Asp Pro  
115 120 125  
Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly Val Asn Asn  
130 135 140  
Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu Gln Ala Val  
145 150 155 160  
Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro Phe Ser Leu  
165 170 175  
Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe Ser Asp Asn  
180 185 190  
Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln Ser Phe Asp  
195 200 205  
Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr Leu Thr Pro  
210 215 220  
Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe Gly Asp Leu  
225 230 235 240  
Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu Glu Arg Thr  
245 250 255  
Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro His Trp Asp  
260 265 270  
Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu Leu Thr Cys  
275 280 285  
Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met Asn Tyr Ser  
290 295 300  
Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu Thr Ala Phe  
305 310 315 320  
Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr Ser Leu Ser Pro  
325 330 335  
Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys Phe Ile Thr Gln  
340 345 350  
Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu Pro Lys Leu Ala  
355 360 365  
Ala Ala Leu Glu His His His His His His  
370 375

(2) INFORMATION FOR SEQ ID NO: 138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleotide
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:  
CTTGGAGGGT GCATAACCAG GGAAT

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(2) INFORMATION FOR SEQ ID NO: 139:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleotide  
10 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

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TGTCCGCTGT GCTCCTGATC  
(2) INFORMATION FOR SEQ ID NO: 140:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleotide  
20 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

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CTATGTCCTT TTGGACTGTT TGGGT  
(2) INFORMATION FOR SEQ ID NO: 141:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 764 base pairs  
(B) TYPE: nucleotide  
30 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGTCCGCTGT GCTCCTGATC CAGCACAGGC GCCCATGCC TCTCCAATT GGGCTAAAGG 60  
CTTGGCCATTG TTCCCTGCACA GCTAACTGCC TGGGTTCATC CTAATCGAGC TGAACACTAG 120  
TCACACTGGTT CCACCGTTCT CTTCCATGAC CCATGGCTTC TAATAGAGCT ATAACACTCA 180  
CTGCATGGTC CAAGATTCCA TTCCCTGGAA TCCGTGAGAC CAAGAACCCC AGGTCAGAGA 240  
ACACAAAGGCT TGCCACCATG TTGGAAGCAG CCCACCCACCA TTTTGGAAAGC AGCCCCGCCAC 300  
TATCTTGGGA GCTCTGGGAG CAAGGACCCC AGGTAACAAT TTGGTGACCA CGAAGGGACC 360  
TGAATCCGCA ACCATGAAGG GATCTCCAAA GCAATTGGAA ATGTTCCCTCC CAAGGCAAAA 420  
ATGCCCCCTAA GATGTATTCT GGAGAATTGG GACCAATTG ACCCTCAGAC AGTAAGAAAA 480  
AAATGACTTA TATTCTTCTG CAGTACCGCC CTGGCCACGA TATCCTCTTC AAGGGGGAGA 540  
AACCTGGCT CCTGAGGGAA CTATAAATTA TAACACCATC TTACAGCTAC ACCTCTTTTC 600  
TAGAAAAGGA GCAAATGGA GTGAAGTGCC ATATTACAA ACTTTCTTTT CATTAAAAGA 660  
CAACTCCCAA TTATGTTAAC AGTGTGATT GTGTTCCCTAC ACGGAAGCCC TCAGATTCTA 720  
CTCCCCACCC CGGGCATCTC CCCTGAATCC CTCCCCAACT TATT 784

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 800 base pairs  
5 (B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

TGTCCGCTGT GCTCCTGATC CAGCACAGGC GCCCATGCC TCTCCAATT GGGCTAAAGG 60  
CTTGGCCATTG TTCCCTGCACA GCTAACTGCC TGGGTTCATC CTAATCGAGC TGAACACTAG 120  
TCACACTGGTT CCACCGTTCT CTTCCATGAC CCATGGCTTC TAATAGAGCT ATAACACTCA 180  
CTGCATGGTC CAAGATTCCA TTCCCTGGAA TCCGTGAGAC CAAGAACCCC AGGTCAGAGA 240  
ACACAAAGGCT TGCCACCATG TTGGAAGCAG CCCACCCACCA TTTTGGAAAGC GGGGGGGCCAC 300  
TATCTTGGGA GCTCTGGGAG CAAGGACCCC CAGGTAACAA TTTGGTGACCA CGAAGGGACC 360  
CTGAATCCGCA ACCATGAAG GATCTCCAAA AGCAATTGGAA ATGTTCCCTC CCAAGGCAAAA 420  
AAATGCCCCCTA AGATGTATTG TGGAGAATTG GGACCAATCT GACCCCTCAGA CAGTAAGAAA 480  
AAAAATGACT TATATTCTTC TGCAGTACCG CCTGGCCATG GATATCCTCT TCAAGGGGGAGA 540  
GAAACCTGGC CTCCCTGAGGG AAGTATAAAT TATAACACCA TCTTACAGCT AGACCTGTTT 600  
TGTAGAAAAG GAGGCAATG GAGTGTGAGTG CCATATTTAC AAACTTCTT TTCATTAAAAA 660  
GACAACCTCGC AATTATGTAA ACAGTGTGAT TGTGTCCTA CAGGAAGCCC TCAGATCTAC 720  
CTCCCCACCC CGGCATCTCC CTGACTCTT CCCCAACTAA TAAGGACCCA CTTCAGCCCCA 780  
10 AACAGTCCAA AAGGACATAG 800